

CLAIMS

What is claimed is:

1. An isolated nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, and complements thereof.
2. A DNA molecule isolated from cotton tissue, said molecule comprising the sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, and complements thereof.
3. A first and a second nucleotide primer sequence which function together in the presence of template cotton plant event 757 nucleic acid sequences in a sample to produce an amplicon diagnostic for the cotton plant event 757, said first and second nucleotide primer sequences being selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20 and SEQ ID NO:21.
4. The first and second nucleotide primer sequence of claim 3, wherein said first nucleotide primer sequence comprises SEQ ID NO: 9 and said second nucleotide primer sequence comprises SEQ ID NO: 10, and wherein said amplicon comprises SEQ ID NO: 1.
5. The first and second nucleotide primer sequence of claim 3, wherein said first nucleotide primer sequence comprises SEQ ID NO: 11 and said second nucleotide primer sequence comprises SEQ ID NO: 12, and wherein said amplicon comprises SEQ ID NO: 2.
6. The first and second nucleotide primer sequence of claim 3, wherein said first nucleotide primer sequence comprises SEQ ID NO: 16 and said second nucleotide primer sequence comprises SEQ ID NO: 17, and wherein said amplicon comprises SEQ ID NO: 3.
7. The first and second nucleotide primer sequence of claim 3, wherein said first nucleotide primer sequence comprises SEQ ID NO: 18 and said second nucleotide primer sequence comprises SEQ ID NO: 19, and wherein said amplicon comprises SEQ ID NO: 3.
8. The first and second nucleotide primer sequence of claim 3, wherein said first nucleotide primer sequence comprises SEQ ID NO: 20 and said second nucleotide primer sequence comprises SEQ ID NO: 21, and wherein said amplicon comprises SEQ ID NO: 4.
9. The first and second nucleotide primer sequence of claim 3 wherein said first nucleotide primer sequence is complementary to a cotton plant genome sequence flanking the point of insertion of a heterologous DNA sequence inserted into the cotton plant genome, and said

second nucleotide primer sequence is complementary to a part of the heterologous DNA
5 sequence inserted into the cotton plant genome, and wherein said amplicon is diagnostic for
said event 757.

10. The first and second nucleotide primer sequence of claim 3 wherein said first nucleotide
primer sequence is complementary to a first sequence inserted into the cotton plant genome
and said second nucleotide primer sequence is complementary to a second sequence inserted
into the genome which is other than said first sequence, and wherein said amplicon is
5 diagnostic for said event 757.

11. The first and second nucleotide primer sequence of claim 10, wherein said first
nucleotide primer sequence comprises SEQ ID NO: 16 and said second nucleotide primer
sequence is selected from the group consisting of SEQ ID NO: 17, SEQ ID NO: 19, and SEQ
ID NO: 21.

12. The first and second nucleotide primer sequence of claim 10, wherein said first
nucleotide primer sequence comprises SEQ ID NO: 18 and said second nucleotide primer
sequence is selected from the group consisting of SEQ ID NO: 19 and SEQ ID NO: 21.

13. The first and second nucleotide primer sequence of claim 10, wherein said first
nucleotide primer sequence comprises SEQ ID NO: 21 and said second nucleotide primer
sequence is selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 18, and SEQ
ID NO: 16.

14. The first and second nucleotide primer sequence of claim 10, wherein said first
nucleotide primer sequence comprises SEQ ID NO: 19 and said second nucleotide primer
sequence is selected from the group consisting of SEQ ID NO: 18 and SEQ ID NO: 16.

15. A method of detecting the presence of cotton plant event 757 nucleic acid sequences in
a sample comprising the steps of:

- a) contacting said sample with a first nucleotide and a second nucleotide primer
sequence which function together in the presence of template cotton plant
5 event 757 nucleic acid sequences in a sample to produce an amplicon
diagnostic for the cotton plant event 757;
- b) performing a nucleic acid amplification reaction, thereby producing said
amplicon; and
- c) detecting said amplicon.

16. The method of claim 15 wherein said first and second nucleotide primer sequences are
selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ

ID NO: 12, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20 and SEQ ID NO: 21.

17. The method of claim 15 wherein said amplicon comprises a nucleotide sequence comprising at least 11 consecutive nucleotides selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, and complements thereof.

18. An isolated nucleotide sequence comprising the amplicon produced by the method of claim 15.

19. A nucleic acid detection kit for use in identifying the presence of cotton plant event 757 nucleic acids in a sample comprising

- a) a probe which is or is complementary to a part of the heterologous DNA sequence inserted into the genome of cotton plant event 757, said probe comprising at least 11 or more consecutive nucleotides, said consecutive nucleotides being selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, and complements thereof;
- b) reagents necessary for detecting the binding of said probe to the heterologous DNA sequence inserted into the genome of cotton plant event 757; and
- c) instructions for use packaged together in said kit.

20. A method of detecting the cotton plant event 757 nucleic acid sequences in a sample comprising

- a) contacting the sample with a polynucleotide probe sequence that binds under stringent conditions with said nucleic acid sequences;
- b) subjecting the sample and probe to said stringent conditions; and
- c) detecting the binding of the probe to said nucleic acid sequences.

21. An isolated nucleic acid sequence comprising a cotton plant genome-inserted heterologous DNA sequence junction present in cotton plant event 757 comprising a sequence of 11 consecutive nucleotides selected from the group consisting of SEQ ID NO: 1 or SEQ ID NO: 2.

22. A method of detecting the presence of a DNA molecule corresponding to a DNA sequence in cotton plant event 757 or homozygous or heterozygous progeny thereof in a sample, the method comprising:

- a) contacting the sample with a probe that does not bind under stringent conditions with DNA from a cotton plant other than said event ;
- b) subjecting the probe and sample to stringent conditions; and

- c) detecting the binding of the probe to said DNA sequence.

23. A method of determining the zygosity of a cotton plant genome comprising a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, and complements thereof, said method comprising the steps of:

- a) contacting a sample comprising DNA obtained from said cotton plant with a first and a second nucleotide primer sequence that, when used in a nucleic acid amplification reaction with a first template comprising cotton plant event 757 DNA, produces a first amplicon that is diagnostic for cotton plant event 757;
- b) performing a nucleic acid amplification reaction with said first and second nucleotide primer sequences and said first template, thereby producing said first amplicon;
- c) detecting said first amplicon;
- d) contacting said sample with a first and a third nucleotide primer sequence that, when used in a nucleic acid amplification reaction with a second template comprising cotton plant DNA other than event 757 DNA, produces a second amplicon that is diagnostic for other than cotton plant event 757;
- e) performing a nucleic acid amplification reaction with said first and third nucleotide primer sequences and said second template, thereby producing said second amplicon; and
- f) detecting said second amplicon,

wherein detection of said second amplicon is diagnostic for the zygosity of said cotton plant genome.